



# Blast 2 Sequences results

PubMed

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BLAST

OMIM

Taxonomy

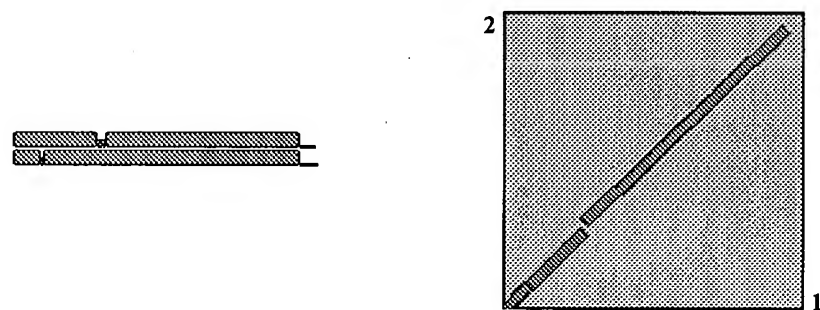
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter: ☒ View option: **Standard**  
 Masking character option: **X for protein, n for nucleotide** Masking color option: **Black**  
☐ Show CDS translation **Align**

Sequence 1: **lcl|seq\_1**  
 Length = 183 (1 .. 183)

Sequence 2: **gi|1717863|sp|P52491|UBC12\_YEAST|NEDD8-conjugating enzyme UBC12 (RUB1-conjugating enzyme) (RUB1-protein ligase) (Ubiquitin carrier protein 12).**  
 Length = 188 (1 .. 188)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 153 bits (386), Expect = 5e-36  
 Identities = 76/179 (42%), Positives = 114/179 (63%), Gaps = 8/179 (4%)

```
Query 1  MIKLFSLKQQKKEESAGGTKGSSKKASAAQLRIQKDINELNLPKTCDISF-----SDP  54
          M+KL L+++K++E   +   SAA++R+++D++ L+LP T ++   +D
Sbjct 1  MLKLRQLQKKKQKENE--NSSSIQPNLSAARIRLKRDLSDLPTVTNLNVITSPDSADR  58

Query 55  DLLNFKLVICPDGEFYKSGKFVFSFKVGQGYPHDPPKVKCETMVYHPNIDLEGNVCLNI  114
          ++++ PDEG+Y  G  F+   + YP +PPKV C  ++HPNIDL+GNVCLNI
Sbjct 59  SQSPKLEVIVRPDEGYNYGSINFNLDNEVYPIEPPKVCLKKIFHPNIDLKGNVCLNI  118

Query 115 LREDWKPVLTINSIIYGLQYLFLEPNPEDPLNKEAAEVLQNNRRLFEQNVQSRMGGYI  173
          LREDW P L + SII GL +LFLEPNP DPLNK+AA++L   + F + V+ +M GG I
Sbjct 119 LREDWSPALDLSIITGLLFLFLEPNPNLNDPLNKDAAKLLCEGEKEFAEAVRLTMSGGSI  177
```

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H  
 0.318 0.138 0.411

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 302

## Blast Result

Number of extensions: 163  
Number of successful extensions: 2  
Number of sequences better than 10.0: 1  
Number of HSP's gapped: 1  
Number of HSP's successfully gapped: 1  
Length of query: 183  
Length of database: 1,238,154,749  
Length adjustment: 125  
Effective length of query: 58  
Effective length of database: 1,238,154,624  
Effective search space: 71812968192  
Effective search space used: 71812968192  
Neighboring words threshold: 9  
X1: 16 ( 7.3 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 41 (21.7 bits)  
S2: 74 (33.1 bits)

2

# RESULT 1

## UBE2M\_HUMAN

ID UBE2M\_HUMAN STANDARD; PRT; 183 AA.  
AC P61081; O76069; Q8VC50;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ubiquitin-conjugating enzyme E2 M (EC 6.3.2.19) (Ubiquitin-protein  
DE ligase M) (Ubiquitin carrier protein M) (Nedd8-conjugating enzyme  
DE Ubc12).  
GN Name=UBE2M; Synonyms=UBC12;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RA Gong L., Yeh E.T.H.;  
RT "Identification of the activating and conjugating enzymes of the  
RT NEDD8-conjugation pathway.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98361870; PubMed=9694792;  
RA Osaka F., Kawasaki H., Aida N., Saeki M., Chiba T., Kawashima S.,  
RA Tanaka K., Kato S.;  
RT "A new NEDD8-ligating system for cullin-4A.";  
RL Genes Dev. 12:2263-2268(1998)..  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor  
RT vector.";  
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,



Qy	121	CTGAACCTGCCCAAGACGTGTGATATCAGCTTCTCAGATCCAGACGACCTCCTCAACTTC	180
Db	41	LeuAsnLeuProLysThrCysAspIleSerPheSerAspProAspAspLeuLeuAsnPhe	60
Qy	181	AAGCTGGTCATCTGTCCTGATGAGGGCTTCTACAAGAGTGGGAAGTTTGTGTTTCAGTTTT	240
Db	61	LysLeuValIleCysProAspGluGlyPheTyrLysSerGlyLysPheValPheSerPhe	80
Qy	241	AAGGTGGGCCAGGGTTACCCGCATGATCCCCCAAGGTGAAGTGTGAGACAATGGTCTAT	300
Db	81	LysValGlyGlnGlyTyrProHisAspProProLysValLysCysGluThrMetValTyr	100
Qy	301	CACCCCAACATTGACCTCGAGGGCAACGTCTGCCTCAACATCCTCAGAGAGGACTGGAAG	360
Db	101	HisProAsnIleAspLeuGluGlyAsnValCysLeuAsnIleLeuArgGluAspTrpLys	120
Qy	361	CCAGTCCTTACGATAAACTCCATAATTTATGGCCTGCAGTATCTCTTCTGGAGCCCAAC	420
Db	121	ProValLeuThrIleAsnSerIleIleTyrGlyLeuGlnTyrLeuPheLeuGluProAsn	140
Qy	421	CCCGAGGACCCACTGAACAAGGAGGCCGCAGAGGTCCTGCAGAACAACCGGCGGCTGTTT	480
Db	141	ProGluAspProLeuAsnLysGluAlaAlaGluValLeuGlnAsnAsnArgArgLeuPhe	160
Qy	481	GAGCAGAACGTGCAGCGCTCCATGCGGGGTGGCTACATCGGCTCCACCTACTTTGAGCGC	540
Db	161	GluGlnAsnValGlnArgSerMetArgGlyGlyTyrIleGlySerThrTyrPheGluArg	180
Qy	541	TGCCTGAAA	549
Db	181	CysLeuLys	183